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SEQUENCE LISTING

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<120> HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

<130> DX0804K

<140> 09/265,540

<141> 1999-03-08

<150> 60/077,329

<151> 1999-03-09

<160> 6

<170> PatentIn version 3.1

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<213> Homo sapiens

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agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact
 120

gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca
 170

Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

1

5

10

agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca
 218

Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr

15

20

25

gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca
 266

Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser

30

35

40

45

acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga
 314

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly

50

55

60

gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg
362

Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu

65

70

75

tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa
410

Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu

80

85

90

ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac
458

Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr

95

100

105

aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc
506

Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser

110

115

120

125

atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct
554

Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro

130

135

140

ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag
602

Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu

145

150

155

gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag
650

Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu

160

165

170

cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca
698

Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro

175

180

185

gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc
746

Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala

190

195

200

205

cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca
794

Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr

210

215

220

gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg
842

Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu

225

230

235

ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc
890

Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe

240

245

250

gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg
938

Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val

255

260

265

gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc
986

Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile

270

275

280

285

agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct
1034

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser

290

295

300

cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca
1084

Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser

305

310

ggtgaagccg agaacctggg ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc
1144

tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgctc tacaagtcta
1204

gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg
1264

gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga
1324

cttcacccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg
1381

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<213> Homo sapiens

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<223> The 'Xaa' at location 146 stands for Thr, Ala, Pro, or Ser.

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<222> (148)..(148)

<223> The 'Xaa' at location 148 stands for Asn, Asp, His, or Tyr.

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 <223> The 'Xaa' at location 171 stands for Arg, or Thr.

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 <222> (214)..(214)
 <223> The 'Xaa' at location 214 stands for Arg, or Lys.

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		20					25						30		

Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	Thr	Asn	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 50 55 60

Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 65 70 75 80

His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 85 90 95

Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 100 105 110

Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 115 120 125

His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 130 135 140

Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 145 150 155 160

Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
 165 170 175

Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 180 185 190

Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 195 200 205

Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 210 215 220

Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe

tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc
145

Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro

35

40

45

ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay
193

Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr

50

55

60

tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac
241

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn

65

70

75

80

tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa
289

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln

85

90

95

gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc
337

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly

100

105

110

cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg
385

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr

115

120

125

aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg
433

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu

130

135

140

gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc
481

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly

145

150

155

160

ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc
529

Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile

165

170

175

gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac
577

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp

180

185

190

aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt
625

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val

195

200

205

gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc
673

Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr

210

215

220

caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag
724

Gln Asn Ser Gly Ala Val Cys

225

230

gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc
784

aaaaggcccc tcagtgcctg tgaagatgta acgggtctca tgggggacgac aagcttattg

844

atttttttct tcaaactaag agtttttctaa tcatacgcgt ttttagaata attctacaga
904

tatgtccccg aaagattaag attttctctta aacactaaaa agacatgtaa ttatttgta
964

gcaaatgggc gtctggcacg cctctgacac tttttcgtca gcagccagga cacgagggtcc
1024

cctccttgat gaagcccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg
1084

gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta
1144

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1204

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<211> 231

<212> PRT

<213> Homo sapiens

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Trp	Phe	Leu	Ser	Cys	Trp	Asn	Val	Thr	Ile	Gly	Pro	Pro	Glu	Ser	Ile
		20						25					30		

Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro
		35					40					45			

Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	Tyr
50						55					60				

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn

65

70

75

80

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
85 90 95

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
100 105 110

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
115 120 125

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
130 135 140

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
145 150 155 160

Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
165 170 175

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
180 185 190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
195 200 205

Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
210 215 220

Gln Asn Ser Gly Ala Val Cys
225 230

<210> 5
<211> 337
<212> PRT
<213> Homo sapiens

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 20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
 35 40 45

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg
 50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
 65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
 85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
 100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
 115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
 130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
 145 150 155 160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
 165 170 175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
 180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
 195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
 210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
 225 230 235 240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
 245 250 255

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
 260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
 275 280 285

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
 290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
 305 310 315 320

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
 325 330 335

Leu

<210> 6
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Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15

Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30

Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
 115 120 125

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140

Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175

Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205

Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala
 210 215 220

Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
 225 230 235 240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe
 245 250 255

Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His
 260 265 270

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu
 275 280 285

Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser
 290 295 300

Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly
 305 310 315 320

Gln Gly Pro Gln Ser
 325